

A Novel Method for Myocardial Image Classification using Data Augmentation

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Abstract—Myocarditis is an important public health concern since it can cause heart failure and abrupt death. It can be diagnosed with magnetic resonance imaging (MRI) of the heart, a non-invasive imaging technology with the potential for operator bias. The study provides a deep learning-based model for myocarditis detection using CMR images to support medical professionals. The proposed architecture comprises a convolutional neural network (CNN), a fully-connected decision layer, a generative adversarial network (GAN)-based algorithm for data augmentation, an enhanced DE for pre-training weights, and a reinforcement learning-based method for training. We present a new method of employing produced images for data augmentation based on GAN to improve the classification performance of the provided CNN. Unbalanced data is one of the most significant classification issues, as negative samples are more than positive, decimating system performance. To solve this issue, we offer an RL-based training method that learns minority class examples with attention. In addition, we tackle the challenges associated with the training step, which typically relies on gradient-based techniques for the learning process; however, these methods often face issues like sensitivity to initialization. To start the BP process, we present an improved differential evolution (DE) technique that leverages a clustering-based mutation operator. It recognizes a successful cluster for DE and applies an original updating strategy to produce potential solutions. We assess our suggested model on the Z-Alizadeh Sani myocarditis dataset and show that it outperforms other methods.

Keywords—Myocarditis; generative adversarial network; data augmentation; differential evolution

I. INTRODUCTION

Myocarditis is a type of cardiovascular disease in which the heart muscle cells inflame and is pathologically specified as inflammatory infiltrates of the myocardium with mononuclear cells. The clinical expressions of myocarditis range from asymptomatic states to cardiac arrest, arrhythmias, and cardiogenic shock [1], [2]. Viral infections are the most critical causes of myocarditis, with recent meta-analyses indicating its pervasiveness among COVID-19 infected patients [3]. Epidemiological studies inform 10.2 to 105.6 cases per 100,000 worldwide and an estimate of 1.8 million annually. In 2017, the global number of myocarditis-related deaths was gauged to be approximately 46,486 cases [4]. Despite passing several centuries since the recognition of the myocardial disease, helpful treatment approaches are yet to be conducted due to several causes, including insensitivity to diagnostic tests and complicated relations between maladaptive and adaptive immune reactions [5], [6]. Current development in the genetic

basis of immune-mediated heart disease and animal analyses supplied vital information in curing this disease [7].

In medical imaging, CNNs are vital in conducting analysis and predicting various health outcomes. Nevertheless, it is a fact that these models struggle with performance issues when they are not sufficiently balanced. So, a compelling need for more robust methods to enhance their performance is required [8]. Existing methods to improve the performance of CNN models in the medical domain include domain adaptation and transfer learning [9]. However, a significant limitation in these methods is the lack of pre-trained models available on extensively annotated medical datasets, which is a critical requirement to train these models effectively. In the absence of such pre-trained models, researchers often resort to traditional transformations, such as rotation, translation, flipping, shearing, and scaling. While these transformations have been successfully applied to many medical datasets, they are not universally applicable. Some datasets are resistant to these transformations, as applying them may alter or compromise the properties of the annotated data. Certain transformations may cause image duplicity. This means that an image and its transformed counterpart are seen by the model as two distinct images. This misjudgment by the model can cause overfitting, where the model is overly calibrated to the training dataset and performs poorly on unseen data. Considering these challenges, there is an urgent need for innovative and effective solutions to enhance the performance of CNN models in the medical domain. Current research should focus on developing new methods that can be universally applied to diverse medical datasets without compromising the integrity of the data and without leading to model overfitting. Such methods will significantly improve the applicability and accuracy of CNN models in medical imaging analysis, leading to better healthcare outcomes.

So far, GANs [10] have achieved much attention in academics and industry for their usefulness in neutralizing domain changes and developing new image instances [11]. GAN models have attained modern efficiency in numerous image generation studies, such as text-to-image synthesis [12], [13], super-resolution [14], and image-to-image translation [15]. Recently it is also being utilized in the medical area [16]. Recent research has been on utilizing GAN in medical augmentation [17] and image segmentation [18]. However, a notable drawback with some of these applications is that they involve offline augmentation, which increases the size of the dataset to enhance model performance. This process can be resource-intensive and time-consuming, making it less suitable

for applications where speed and efficiency are crucial. In contrast, online augmentation methods keep the dataset size constant. During each mini-batch iteration, a fraction of the original images is kept, and the rest is replaced with GAN-generated images. This approach helps maintain a balance between performance improvement and computational efficiency, without the need for expanding the dataset significantly [19].

Deep learning models have played a transformative role in various applications [20], [21], [22]. They leverage complex algorithms that adjust their internal parameters, typically referred to as weights, to minimize the difference between their predictions and actual outputs. To achieve this, a learning process based on the backpropagation of errors is often employed, which adjusts the model's weights based on the calculated gradients of the loss function. However, these gradient-based optimization techniques are not without their limitations. One major vulnerability is their sensitivity to the initialization of the weights. If the initial weights are not set appropriately, these algorithms can converge to local minima, resulting in sub-optimal solutions. This is a standard issue encountered in classification works, where the objective is to categorize inputs into distinct classes. In light of these challenges, researchers have turned their attention to meta-heuristic algorithms [23], which offer alternative methods for optimization. These algorithms provide a more global approach to searching the solution space and are less susceptible to the problem of local minima [24]. One such powerful meta-heuristic algorithm is DE. It has been successfully utilized for a plethora of optimization issues [25]. The DE process involves three essential steps: mutation, crossover, and selection. A new solution is created during the mutation stage. Next, in the crossover phase, the newly created mutation vector is combined with the current vector, introducing diversity into the solution set. Finally, the selection phase evaluates all solutions and selects the best ones to pass into the next iteration. The use of DE in deep learning models could provide a robust alternative to traditional gradient-based optimization methods, mitigating the issues of weight initialization and local minima. Integrating DE into the training of deep models, it could potentially improve their performance, especially in challenging applications like medical image analysis. Consequently, the practical implications of this approach could be enormous, making it an exciting area for future research and development [26].

Imbalance in the categories can have an adverse effect on performance, which is the result of one category having more data than the other [27]. Because of its rarity and volatility, the minority example may be more difficult to identify than the majority example. The data level and algorithmic level are two methods for addressing the imbalance problem. At the data level [28], over-sampling minority or under-sampling majority classes may equilibrate the dispersion of classes, yet carry the hazards of over-fitting and information loss. These techniques provide promising ways to address the class imbalance problem. However, each method has its strengths and limitations, and their effectiveness can vary depending on the specific dataset and application. Consequently, it is crucial to carefully consider the nature of the imbalance problem and the

requirements of the specific application when selecting an appropriate method. A well-chosen strategy for handling class imbalance can significantly improve model performance, particularly in identifying the important but often overlooked minority classes. Using Deep Reinforcement Learning (DRL) has been confirmed to have success in a variety of spheres, enhancing the performance of classification systems through eliminating noisy data and heightening features. However, the computational time increases due to the intricate simulations between agents and environments. Some researchers have used DRL to improve classifiers, and an ensemble pruning approach has also been developed. Despite these advancements, the use of DRL in imbalanced classifications, especially in medical imaging, remains minimally investigated.

As far as we know, three deep network-based articles have been presented to diagnose myocarditis. Sharifrazi et al. [29] presented a three-step method using CNN and the k-means algorithm for myocardial image classification. In this research, images embedded in a vector were clustered using the k-means algorithm in four clusters, followed by a CNN to classify four clusters separately. Eventually, a voting system was employed to assign every image to its corresponding class. The method's fundamental flaw was that it embedded the images in a vector for the k-means algorithm, resulting in missing pixels surrounding a special pixel. Moravvej et al. [30] considered a CNN-based model that used the ABC algorithm as weight initialization of the model and reinforcement learning to solve the imbalanced classification problem. Danaei et al. [31] imitated the method presented by [30] except that they used an improved ABC algorithm for weight initialization. The ABC algorithm often requires many iterations to converge to an optimal solution, making it less efficient than some other optimization algorithms, especially when dealing with high dimensional problems. As the dimensionality of the problem increases, the performance of the ABC algorithm tends to deteriorate, making it less suitable for high-dimensional problems or very complex datasets.

In this article, we offer an automatic method for myocarditis diagnosis. Our proposed model contains a CNN and a feed-forward network to predict their similarity. The main contribution of this article is as: 1) We consider a deep convolutional GAN model effective for online augmenting, generating images allowed in regularization that reduces the over-fitting and enhances the accuracy of the model, 2) We come up with a better DE algorithm based on clustering for initializing weights. This supports us in identifying a likely region for the commencement of the BP algorithm on CNN and feed-forward networks. The mutation operator chooses the most suitable or almost suitable solution from the superior cluster to accomplish this as the primary solution. An updated strategy is then implemented to create potential solutions, and 3) We provide a reinforcement learning algorithm for the classification problem inspired by [30] in order to address imbalanced classification.

The remainder of this article is set as follows. Section II presents our proposed myocarditis diagnosis method, while Section III illustrates experimental results. Eventually, Section IV presents a conclusion of the paper.

II. PROPOSED MODEL

As illustrated in Fig. 1, we employ a deep model for the binary classification of myocardial images. Our model gains a CMR image as input and passes it to a CNN, followed by a Softmax layer at the end serving as the final decision-maker. We use a GAN-based method for online data augmentation, rising the model performance for classification. The proposed model incorporates a clustering-based differential evolution algorithm to find the initial seeds of the network weights while using an RL-based algorithm to handle class imbalance.

A. Online Data Augmentation

Data augmentation is an indispensable tool for training deep models. More recent advances have been made to discover an optimal augmentation policy in image classification. Nevertheless, the current methods uncovered two critical points related to data augmentation. One is that most current augmentation approaches are offline, which separates learning procedures from their use. The techniques that are taught during training remain consistent and are not changed based on the current state of the training model. These techniques depend on image processing functions that maintain class details. Applying offline techniques to new projects may need domain knowledge [32], [33].

To handle the problems above, we present an online data augmentation using a GAN-based model, trying to minimize the overfitting and enhance the performance of the proposed CNN architecture. The input to the second layer of the generator comprises the characteristics determined by the penultimate layer of the discriminator to recreate the original data. Specifically, the generator uses two inputs: random noise, which is utilized to generate real-like examples as standard GAN, and the actual data features used for reconstruction. Fig. 2 shows the proposed GAN, which shows how the process works. The generator input is manifested by the output of the

flatten layer of the discriminator, as shown by the faint black dotted line, when utilizing real data for reconstruction. The linear layer is not considered when the generator reconstructs real data [34].

B. Pre-training Phase

Deep network weight initialization is a critical component of deep models. Inaccurate initial values can sometimes cause the model to fail to converge. In this article, we initialize the weights of the CNN, and feed-forward neural network. For this, we introduce an enhanced DE method that is boosted by a clustering scheme and a novel fitness function. In our enhance DE algorithm, we employ a clustering-based mutation and updating scheme to improve the optimisation performance.

The mutation operator, inspired by the work in [35], identifies a promising region within the search space. The population P at the current point is divided into k clusters using the k-means clustering method, with each cluster representing a different segment of the search space. The number of clusters is determined by selecting a random integer from the range [2, N]. After the clustering process, the most optimal cluster is deemed to be the one with the lowest average fitness among its samples.

The suggested mutation based on clustering is described as follows:

$$\vec{v}^{clu}_i = \overline{win}_g + F(\vec{x}_{r_1} - \vec{x}_{r_2}), \quad (1)$$

where \overline{win}_g is the most acceptable solution in the promising region, and $\vec{x}_{r_1,g}$ and $\vec{x}_{r_2,g}$ are two randomly determined candidate solutions from the current population. It should be noted that \overline{win}_g is not always the population's most acceptable solution. The clustering-based mutation procedure is implemented M times.

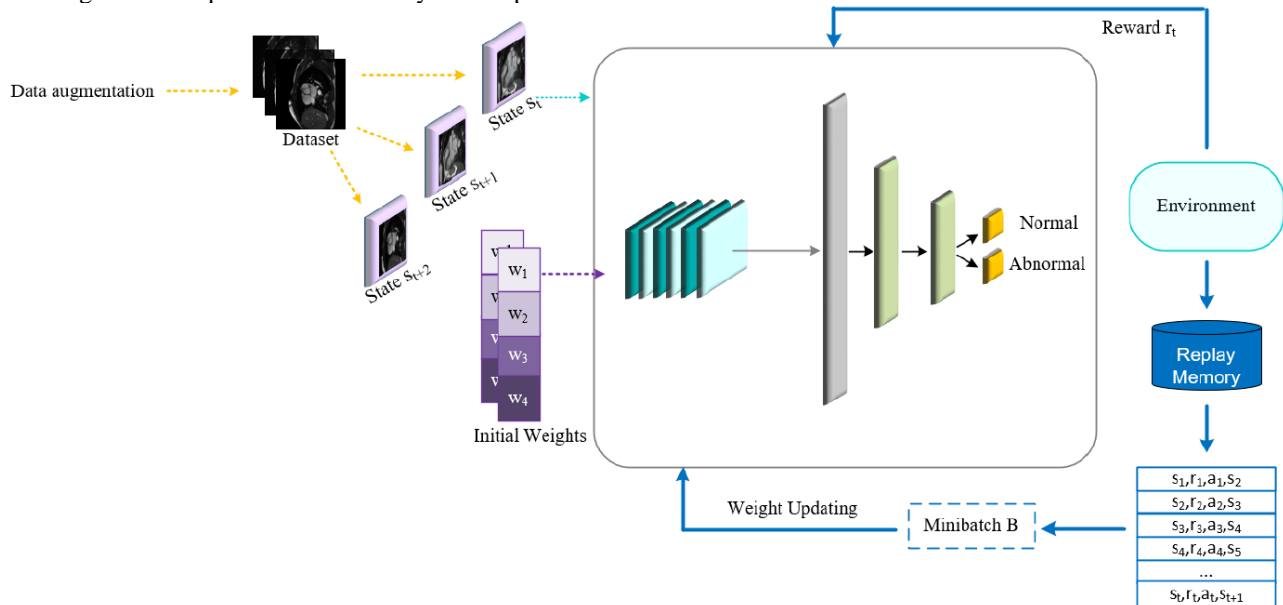


Fig. 1. Outline of the proposed method.

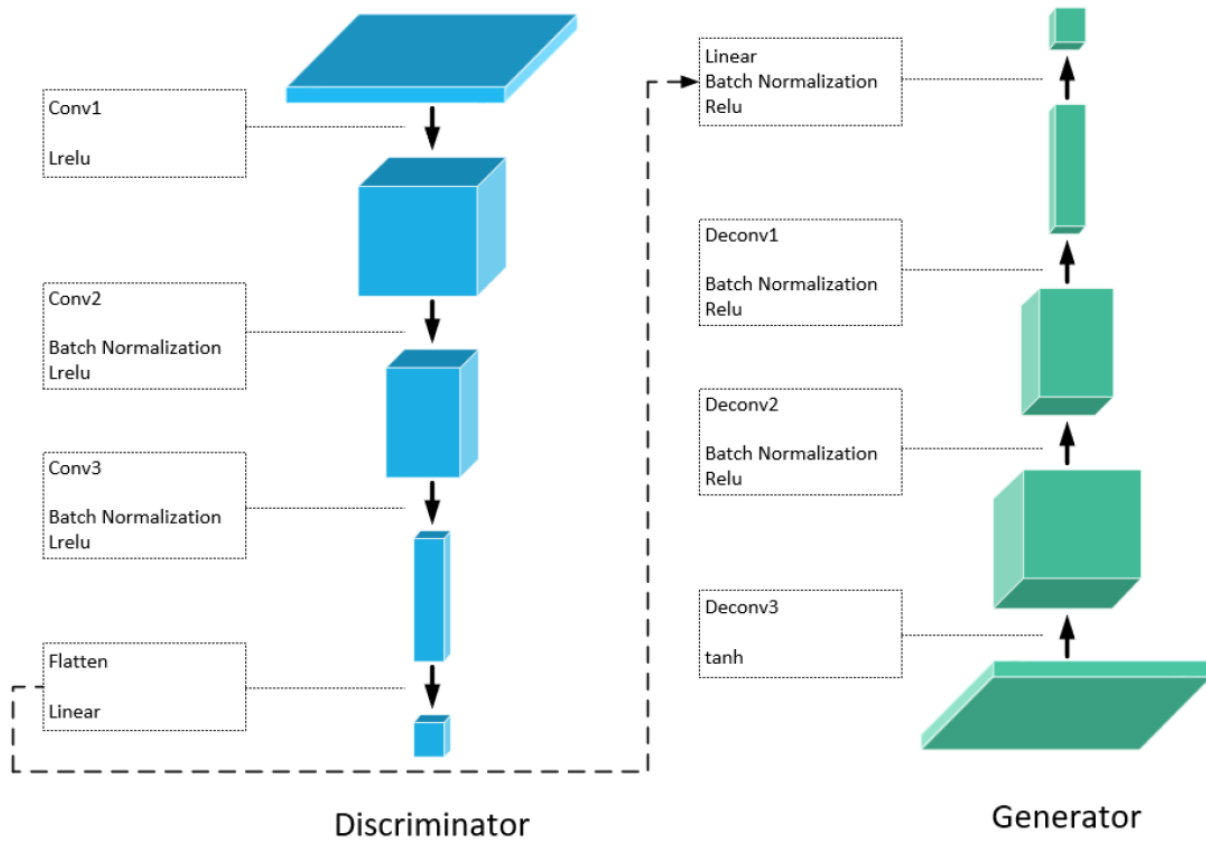


Fig. 2. The proposed GAN architecture for generating images.

The current population is updated when M new solutions have been provoked through clustering-based mutation. The steps are as follows:

- Selection: Produce k random individuals as the starting points for the k-means algorithm;
- Generation: Obtain M solutions utilizing clustering-based mutation and designate them as set v^{clu} ;
- Replacement: Draw M solutions randomly and classify them as B.
- Update: The most helpful M solutions from the union of $vclu$ and B were established as B'. The final population is evaluated as $(P - B) \cup B'$.

The encoding method we use in our research tries to put the CNN and feed-forward weights into a vector that show the candidate solution in the improved DE. It's hard to give exact weights, but after a few trials, we came up with a way to encode that is as accurate as possible. Fig. 3 shows an example of how to encode a feed-forward network with three hidden layers and a three-layer CNN network with three filters in each layer. It is important to remember that all weight matrices in the vector are reserved as rows.

To compute the efficacy of a solution in the improved DE algorithm, the fitness factor is expressed as follows:

$$Fitness = \frac{1}{1 + \sum_{i=1}^N (y_i - \hat{y}_i)^2} \quad (2)$$

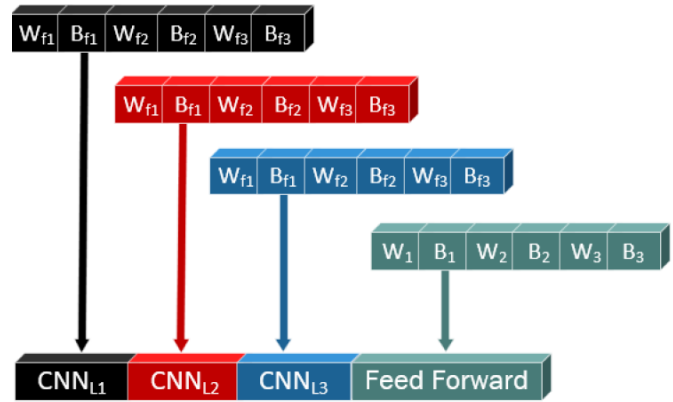


Fig. 3. Placing weights in a vector.

The target and projected labels for the i-th set of data are y_i and \hat{y}_i , respectively, and N shows the number of instances.

C. Classification

Our approach to addressing the issue of imbalanced data volumes in our classes involves the utilization of a RL based algorithm [30]. In our training dataset, each CMR image represents a state within the environment, while the network functions as the agent responsible for performing a series of classifications on all CMR images. The agent's prediction of the class label for a given CMR image can be viewed as an action, where the image observed at time-step t is denoted as state s_t and the performed classification is labeled as a_t . In response,

the environment provides a reward r_t to guide the agent's learning process. To ensure appropriate guidance, the reward values are assigned in a manner that assigns a lower absolute value to the majority class when compared to the minority class. The reward function is:

$$r_t(s_t, a_t, l_t) = \begin{cases} +1, a_t = y_t \text{ and } s_t \in D_H \\ -1, a_t \neq y_t \text{ and } s_t \in D_H \\ \lambda, a_t = y_t \text{ and } s_t \in D_S \\ -\lambda, a_t \neq y_t \text{ and } s_t \in D_S \end{cases} \quad (3)$$

where D_S , and D_H represent the majority ("sick") and minority ("healthy") classes, respectively. Correctly/incorrectly classifying a sample from the majority class yields a reward of $+\lambda/-\lambda$, where $0 < \lambda < 1$.

III. EXPERIMENTAL RESULTS

To assess the proposed model, we designed several experiments. We utilize k-fold cross-validation for experiments, with $k = 5$, meaning the dataset is broken up into k groups. Each time, one fold is chosen to be tested and the rest are used for training. This process is repeated k times. With this technique, every sample can be used once for test and $k - 1$ times for training. We report every result as $M \pm S$, where M and S are the mean and standard deviation of performed experiments for $k - 1$ times.

The first experiment compares the proposed model with three deep learning-based models, CNN-KCL [29], RLMD-PA [30], and Danaei et al. [31]. The evaluation results for the Z-Alizadeh Sani myocarditis dataset using standard performance metrics are displayed in Table I. As the results indicate, the proposed model performs more satisfactorily than CNN-KCL, which decreases error by more than 42% in all criteria. Also, the maximum value of all measures in CNN-KCL has a somewhat high difference compared to the proposed model, for example, in the two criteria of F-measure and Recall, the difference is about 13% and 9%. RLMD-PA acts better to an extent than CNN-KCL, with an improvement of 60%, showing reinforcement learning employed in it can prevent imbalanced data. However, the proposed model acts more robust than RLMD-PA, with about 45% of headway, because GAN used as data augmentation can improve imbalance as much as possible. Proposed without GAN has the same structure as the proposed model but doesn't use GAN as data augmentation. The comparison of these two models shows that the data augmentation trick improved the model by approximately 40%. To investigate the quality of the images generated by the proposed, we select six samples randomly and show them in Fig. 4. We can see that the samples produced by the proposed GAN have relatively high quality.

A. Examination of other Metaheuristic Methods for the Algorithm

In the suggested model, the backpropagation process is influenced by the improved DE method for initializing value. For comparison of improved DE in our model, we utilized six algorithms, including, GDA [36], OSS [37], BR [38], BA [39], COA [40] and original DE [41]. Table II provides an overview of the performance measures used in these comparisons. Metaheuristic algorithms act weaker than the proposed model in terms of accuracy, recall, and F-measure scores. It is significant to note that the improved DE algorithm surpassed all metaheuristic algorithms to reduce the error in the recall and F-measure criterion by more than 38% and 36%, respectively.

1) *Analysis of pre-trained models:* The proposed approach uses a CNN as feature extractors. It is interesting to investigate the effect of transfer learning by utilizing pre-trained models such as AlexNet [42], GoogleNet [43], ResNet [44], DenseNet [45], and MobileNet [46] as feature extractors. The performance metrics of these comparisons are summarized in Table III. As can be seen, replacing CNN trained from scratch by the pre-trained models hurts performance. In particular, training CNNs from scratch improves Recall and F-measure error by more than 60% and 67%, respectively. This stems from the fact that transfer learning models perform reasonable on wide range of images however they lack the necessary specialty for specific problems such as myocardial diagnosis.

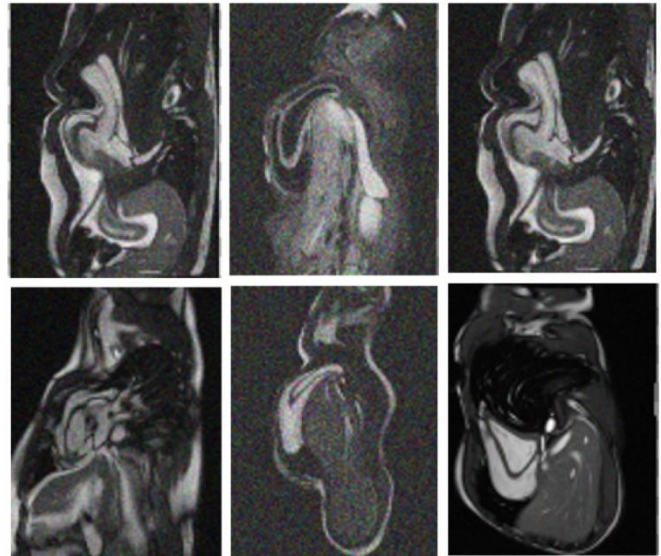


Fig. 4. Examples of images generated by the generator.

TABLE I. RESULTS OF DEEP LEARNING ON THE Z-ALIZADEH SANI MYOCARDITIS DATASET

	Accuracy	Recall	Precision	F-measure
CNN-KCL [29]	0.812 ± 0.015	0.736 ± 0.051	0.743 ± 0.033	0.741 ± 0.021
RLMD-PA [30]	0.881 ± 0.026	0.849 ± 0.013	0.818 ± 0.043	0.829 ± 0.02
Danaei et al. [31]	0.881 ± 0.006	0.856 ± 0.026	0.845 ± 0.023	0.821 ± 0.017
Proposed without GAN	0.858 ± 0.023	0.826 ± 0.027	0.804 ± 0.038	0.814 ± 0.027
Proposed	0.908 ± 0.020	.886 ± 0.028	0.871 ± 0.040	0.878 ± 0.025

TABLE II. RESULTS OF METAHEURISTIC ALGORITHMS ON THE Z-ALIZADEH SANI MYOCARDITIS DATASET

	Accuracy	Recall	Precision	F-measure
GDA	0.841 ± 0.019	0.811 ± 0.024	0.781 ± 0.043	0.794 ± 0.021
OSS	0.845 ± 0.011	0.800 ± 0.023	0.794 ± 0.021	0.797 ± 0.026
BR	0.833 ± 0.010	0.783 ± 0.010	0.780 ± 0.042	0.786 ± 0.017
BAT	0.855 ± 0.021	0.798 ± 0.029	0.810 ± 0.019	0.801 ± 0.018
COA	0.849 ± 0.010	0.806 ± 0.006	0.789 ± 0.032	0.790 ± 0.045
DE	0.893 ± 0.014	0.871 ± 0.020	0.852 ± 0.031	0.870 ± 0.019

TABLE III. RESULTS OF VARIOUS PRE-TRAINED MODELS ON THE PROPOSED MODEL

	Accuracy	Recall	Precision	F-measure
AlexNet	0.761	0.682	0.618	0.625
GoogleNet	0.752	0.764	0.651	0.707
ResNet	0.743	0.706	0.645	0.659
DenseNet	0.732	0.720	0.622	0.659
MobileNet	0.763	0.734	0.652	0.706

TABLE IV. RESULTS OF VARIOUS LOSS FUNCTIONS ON THE PROPOSED MODEL

	Accuracy	Recall	Precision	F-measure
WCE	0.801	0.732	0.758	0.744
BCE	0.800	0.805	0.714	0.745
DL	0.806	0.795	0.701	0.715
TL	0.813	0.774	0.710	0.752

2) *Analysis of loss function:* To address data imbalances, conventional methods can be employed, such as adjusting data augmentation techniques and the loss function. Among these approaches, the loss function holds significant importance as it enables the emphasis of the minority class. We aim to use four loss functions, WCE [47], BCE [48], DL [49], and TL [50] to evaluate the proposed model. As we can observe from Table IV, WCE/BCE functions improved the F-measure metric by only 20%/16% despite assigning weights to the samples. The use of focal loss gives the best results for all measures on the Z-Alizadeh Sani myocarditis dataset and yields in particular the best G-means results for this dataset.

3) *Impact of the reward function:* To address the reward assignment in the context of correct and incorrect classifications, the majority and minority classes are assigned rewards of ± 1 and λ , respectively. The value of λ is determined by the ratio of majority to minority samples, with an expected decrease in the optimal value as the ratio increases. To investigate the impact of λ , the performance of the proposed model was evaluated using different values of λ ranging from 0 to 1, with increments of 0.1, while keeping the majority class bonus constant. The results are depicted in Fig. 5. When λ is set to 0, the influence of the majority class becomes negligible, whereas at $\lambda = 1$, both the majority and minority classes have equal impacts. Fig. 5 illustrates that the model's performance reaches its peak at a λ value of 0.6 for all considered metrics. This suggests that the optimal λ value lies between zero and one, rather than at the extremes. However, it should be noted that excessively low values of λ can adversely affect the overall model performance. Therefore, careful consideration is required in choosing λ to strike the right

balance. The results emphasize that the selection of λ significantly influences the performance of the proposed model. The optimal value depends on the relative proportions of the majority and minority samples, and it is crucial to make a thoughtful choice to achieve the best possible results.

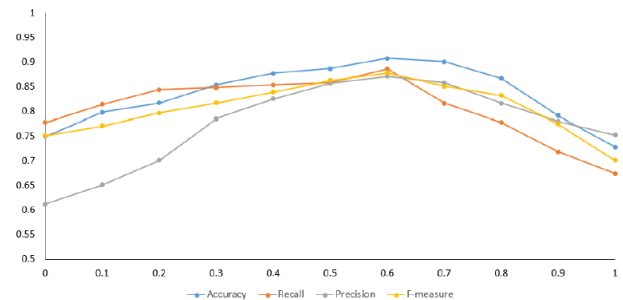


Fig. 5. Performance metrics plotted vs the value of λ in the reward function.

4) *Discussion:* The proposed model has shown excellent results in the task of diagnosing myocarditis on CMR images, outperforming other deep models and pre-trained transfer learning models. The use of data augmentation and RL in the model has addressed the issue of dataset imbalance and improved the model's performance. Additionally, the use of DE pre-training has minimized the risk of the model getting stuck in local optima. However, despite its promising results, the model has some limitations that need to be considered. One of the limitations of the proposed model is that it was trained and tested on a single dataset, the Z-Alizadeh Sani myocarditis CMR dataset, which may limit its generalizability to other datasets with different characteristics. Further validation on other independent datasets is necessary to assess the model's generalizability. Another limitation is that the model

was developed using a retrospective study design, which may introduce biases and limit the ability to draw causal inferences. A prospective study design would be necessary to establish the clinical utility of the model in the diagnosis of myocarditis. Moreover, the model has some technical limitations. For instance, the performance of the model could be influenced by the quality of the input CMR images, which can vary depending on the imaging modality and the specific imaging parameters employed. The performance of the model can also be influenced by the variability in the number and size of myocarditis lesions, which can differ across patients. Future research could overcome these limitations by assessing how well the model performs on a broader range of datasets, including those with a reduced incidence of myocarditis. Furthermore, conducting a performance evaluation of the proposed model in comparison to other deep learning models developed for CMR-based myocarditis diagnosis can provide significant knowledge about the strengths and limitations of different approaches. Lastly, future research could focus on the development of deep learning segmentation methods that can not only detect the existence of myocarditis but also accurately determine the specific location and severity of the condition on CMR images. Such methods could help clinicians make more informed decisions about patient management and treatment.

IV. CONCLUSIONS

We presented an architecture comprising a CNN, a fully-connected decision layer, a generative adversarial network (GAN)-based algorithm for data augmentation, an enhanced DE for pre-training weights, and a RL-based method for training. We proposed an online GAN model that can effectively make synthetic myocardial images. This method of online augmentation using the generated images based on the GAN model increases the accuracy of the test dataset. To protect the proposed model against imbalanced data, we present an RL-based training strategy that focuses on learning minority class examples. We also discuss the training phase, which often involves gradient-based methods, including back-propagation, for the learning process and, as a result, is susceptible to issues such as sensitivity to initialization. In order to start the BP procedure, we provide an enhanced DE method that employs a clustering-based mutation operator. It identifies a winning cluster for the current DE population and develops potential solutions using a new updating strategy. We used the Z-Alizadeh Sani myocarditis dataset to evaluate our proposed method and show that it works better than other methods.

For future work, several aspects can be improved upon or explored further. While our online GAN model has demonstrated effectiveness in generating synthetic myocardial images, it could be refined or adapted for other types of medical images. Experimentation with other types of data augmentation techniques could also prove beneficial. Additionally, the RL-based strategy can be further optimized to ensure more robust handling of imbalanced data. Investigating other advanced optimization techniques for the initialization

process could lead to more efficient learning and overall improved performance. Lastly, applying and testing our proposed architecture on a variety of medical datasets will be critical to understand its versatility and effectiveness in a broader context. The potential of our proposed method is significant, but so is the potential for further enhancements and broader applications.

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